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Run on: July 23, 1999, 11:23:48 ; search time (without a

on 4.5  
8 Compugen Ltd.

C	38	53.4	0.8	2483	5
C	39	53.2	0.8	1385	5
C	40	53	0.8	PCT-US91-03449A-2	1
C	41	53	0.8	US-08-616-844-7	1
C	42	52.6	0.8	6407	4
C	43	52.6	0.8	6407	4
C	44	52.6	0.8	6407	4
C	45	52.4	0.8	6407	4
				US-08-599-654-7	1
				US-08-184-977C-4	1
				US-08-306-691B-4	1
				US-08-845-998-7	1
				US-08-036-555B-21	1
				2003	1

```

Sequence 3, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 42, Appli
Sequence 7, Appli
Sequence 21, Appli

```

8229.332 Million cell updates/

COMMENT

Title:	US-08-956-991-1
Perfect score:	6504
Sequence:	tgcgtggaaqccgaaqcacgg.....
Scoring table:	IDENTITY_NUC
Searched:	176461 seqs, 45838279 residues

```

Title: US-08-956-991-1
perfect score: 6504
Sequence: 1 tgaactgtggccggacacgg. .... .gaaaattggccaaataatatt 6504
Scoring table: IDENTITY_NUC

Searched: 176161 seqs, 45838279 residues

```

```

use : Issued_Patents_NA:*
1: /cgn2_5/prodata/z/ina/5A_COMB.seq:*
2: /cgn2_5/prodata/z/ina/5B_COMB.seq:*
3: /cgn2_5/prodata/z/ina/5C_COMB.seq:*
4: /cgn2_5/prodata/z/ina/5D_COMB.seq:*
5: /cgn2_5/prodata/z/ina/PERTUS_CC_IP.seq:*
6: /cgn2_5/prodata/z/ina/backfiles1.seq:*

```

```

base : Issued_Patents_NA:*
1: /cgn2.5/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2.5/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2.5/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2.5/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2.5/ptodata/2/ina/PCTUS9_CCP.seq:*
6: /cgn2.5/ptodata/2/ina/backfileseq:*

```

SUMMARIES

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
c	1	56.4	1.0	6000	2	US-08-348-005B-5
c	2	66.4	1.0	6000	4	US-08-800-822A-6
c	3	66.4	1.0	6000	5	PCT-US94-10166-5
c	4	62.0	0.9	801	4	US-08-700-379-15
c	5	62.0	0.9	12001	3	US-08-458-560A-11
c	6	62.0	0.9	4257	4	US-08-650-473-1
c	7	61.5	0.9	4403	4	US-08-264-941-1
c	8	61.6	0.9	4403	5	PCT-US91-02147A-1
c	9	60.4	0.9	8438	1	US-07-945-283-1
c	10	60.2	1.026	1	US-07-955-526-6	
c	11	59.4	0.9	12001	3	US-08-458-560A-11
c	12	59.4	0.9	4257	4	US-08-650-473-1
c	13	58.8	0.9	44377	4	US-08-804-227C-7
c	14	56.6	0.9	2823	2	US-08-398-008A-1
c	15	55.6	0.8	43280	4	US-08-804-222C-1
c	16	55.4	0.8	1610	1	US-08-560-051-5
c	17	55.4	0.8	803	1	US-07-928-611-12
c	18	55.4	0.8	1610	1	US-07-928-611-21
c	19	55.4	0.8	803	4	US-07-804-811A-12
c	20	55.4	0.8	1610	4	US-08-487-811A-21
c	21	55.4	0.8	803	5	PCT-US93-07370-12
c	22	55.4	0.8	1610	5	PCT-US93-0770-21
c	23	55.2	0.8	5117	5	PCT-US95-05512-1
c	24	55.0	0.8	936	2	US-08-08-977C-4
c	25	54.2	0.8	5467	1	US-07-745-206A-12
c	26	54.2	0.8	7362	3	US-08-455-503A-12
c	27	54.2	0.8	7175	3	US-08-455-543A-8
c	28	54.2	0.8	1550	4	US-08-600-443B-17
c	29	54.2	0.8	7362	4	US-08-193-078B-7
c	30	54.2	0.8	7175	4	US-08-193-078B-7
c	31	54.2	0.8	7362	4	US-08-223-05C-7
c	32	54.2	0.8	7175	4	US-08-223-05C-8
c	33	54.2	0.8	7352	4	US-08-149-007D-7
c	34	54.2	0.8	7175	4	US-08-149-007D-8
c	35	54.2	0.8	5467	4	US-08-311-353-12
c	36	53.8	0.8	6453	3	US-08-306-691B-4
c	37	53.4	0.8	2483	2	US-08-640-040A-3

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: J. MARK HAND  
 STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
 CITY: RAILWAY  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07055-0900  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348,005B  
 FILING DATE: 08-SEP-1993  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/122,032  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAND, J. MARK  
 REGISTRATION NUMBER: 35,545  
 REFERENCE/DOCKET NUMBER: 189421A  
 TELECOMMUNICATION INVENTION:  
 TELEPHONE: 908-594-3441  
 TELEFAX: 908-594-4720  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6000 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-348-005B-6

Query Match 1.0%; Score 66.4; DB 2;  
 Best Local Similarity 47.7%; Pred. No. 7.5e-07;  
 Matches 227; Conservative 0; Mismatches 246  
 Qy 3597 tacccctggacaaacctgtatagaatgtttcatcgtggatcgctg  
 Db 1721 TACGGGGAGGACCTGAGCCAACAGGGAGACGCCCTTC  
 Qy 3657 cggccgcacgggccttttcgttgcggaaatcatcaccacc  
 Db 1781 CGCAGGGCTGGGCCTACCCCCGTTGGCGGCAGGCC  
 Qy 3717 agttaccccccggaaaatcccaaggccatggccacatcccc

```

0000;
3: Gabs 1
ccctgttaac 36556
|||_ccccgcrcg 1780
atgtgcc 3716
||ccAAACCG 1840
aaatatcc 3776

```



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## OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 10:47:22 ; Search time 1887.56 Seconds  
(without alignments)  
12516.755 Million cell updates/sec

Title: US-08-956-991-1

Perfect score: 1 tgactqagggccggaggacgg.....gaaaatttgc当地atattt 6604

Sequence: IDENTITY\_NUC

Scoring table: 808301 seqs., 1788773984 residues

Database: GenEmpl:\*

1: gb\_bal:\*

2: gb\_ba2:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_p11:\*

9: gb\_p12:\*

10: gb\_p11:\*

11: gb\_pr2:\*

12: gb\_pr3:\*

13: gb\_ro:\*

14: gb\_st:\*

15: gb\_sy:\*

16: gb\_un:\*

17: gb\_v1:\*

18: gb\_htg:\*

19: em\_bai:\*

20: em\_fun:\*

21: em\_hum:\*

22: em\_hum2:\*

23: em\_in:\*

24: em\_om:\*

25: em\_or:\*

26: em\_ov:\*

27: em\_pat:\*

28: em\_ph:\*

29: em\_p1:\*

30: em\_ro:\*

31: em\_sy:\*

32: em\_un:\*

33: em\_v1:\*

34: em\_htg:\*

35: em\_sts:\*

36: gb\_bal:\*

37: gb\_ba2:\*

38: gb\_sts:\*

39: gb\_p11:\*

40: gb\_p12:\*

41: gb\_p11:\*

42: gb\_pr2:\*

43: gb\_pr3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match Length	DB ID	Description

## ALIGNMENTS

RESULT	1	AF023450	6413 bp	mRNA	PRI	02-JUN-1998
LOCUS		AF023450		Homo sapiens		
DEFINITION				CHD2-52 Down syndrome cell adhesion molecule (DSCAM)		
ACCESSION				mRNA, complete cds.		
NID				AF023450		
KEYWORDS						
SOURCE				human.		
ORGANISM				Homo sapiens		
REFERENCE				Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS				(bases 1 to 6413)		
TITLE				Kanakawa, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E. and Korenberg, J.R.		
JOURNAL				DSCAM: a Novel Member of the Immunoglobulin Superfamily Maps in a Down Syndrome Region and is Involved in the Development of the Nervous System		
REFERENCE				Unpublished		
AUTHORS				2 (bases 1 to 6413)		
TITLE				Yamakawa, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E. and Korenberg, J.R.		
JOURNAL				Direct Submission		

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OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 10:47:22 : Search time 1887.56 Seconds  
(without alignments)  
12516.755 Million cell updates/sec

Title: US-08-956-991-1  
Perfect score: 6604  
Sequence: tggactggccggagcacqg.....gaaaattggccaaatataatt 6604

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 1788773984 residues

database : GenEmbl:\*

1: qb\_bail:\*

2: qb\_baz:\*

3: qb\_in:\*

4: qb\_om:\*

5: qb\_ov:\*

6: qb\_Pat:\*

7: qb\_ph:\*

8: qb\_st:\*

9: qb\_p12:\*

10: qb\_Pf:\*

11: qb\_p2:\*

12: qb\_p3:\*

13: qb\_ro:\*

14: qb\_sc:\*

15: qb\_sy:\*

16: qb\_up:\*

17: qb\_vl:\*

18: qb\_htc:\*

19: em\_ba:\*

20: em\_fun:\*

21: em\_hum1:\*

22: em\_hum2:\*

23: em\_in:\*

24: em\_om:\*

25: em\_or:\*

26: em\_ov:\*

27: em\_pat:\*

28: em\_ph:\*

29: em\_pl:\*

30: em\_ro:\*

31: em\_sy:\*

32: em\_un:\*

33: em\_vl:\*

34: em\_htc:\*

35: em\_sts:\*

36: qb\_bail:\*

37: qb\_baz:\*

38: qb\_sts:\*

39: qb\_p11:\*

40: qb\_p12:\*

41: qb\_prl:\*

42: qb\_pr2:\*

43: qb\_pr3:\*

ALIGNMENTS

RESULT 1

AF023450 AF023450 LOCUS AF023450 mRNA DEFINITION Homo sapiens CHP2-52 Down syndrome cell adhesion molecule (DSCAM)

ACCESSION AF023450 NID 93169767

KEYWORDS SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo; I. (bases 1 to 613)

REFERENCE Lyons, G.E., and Korenberg, J.R.

AUTHORS Yamakawa, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E., and Korenberg, J.R.

TITLE DSCAM: a Novel Member of the Immunoglobulin Superfamily Maps in a Down Syndrome Region and is Involved in the Development of the Nervous System

Unpublished

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	6212	94.1	6413	11 AF023450







OM of: US-08-956-991-2 to: N\_Geneseq\_34: \* out\_format : pfs

Date: Jul 23, 1999 11:23 AM

About: Results were produced by the GenCore software, version 4.5., copyright (c) 1993-1998 Compugen Ltd.

#### Command line parameters:

```
-MODEL=frame+p2n model -DEV=x1P
-O=/cgn2.1/USPto_spool/MS08956991/runat_23071999-094001_14137/app_query.fasta.1
-DB=N_Geneseq_34 -QMT=fastap -SUFFIX=rng -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=.000
-OGAPOP=.500 -OGAPEXT=.500
-FGAPOP=.000 -FGAPEXT=.000
-DELOP=.000 -DELEXT=.000
-TRANS-human40 -CDI=45 -LIST=45 -DOCALN=1 -MATRIX=pam150
-ALIGN=15 -MODE=LOCAL -OUTFM=PFS -NORM=stat -USER=US08956991
-NCPU=6 -ICPU=3 -WAIT -THREADS=1
```

#### Search information block:

Query: US-08-956-991-2  
Query length: 1910

Database: N\_Geneseq\_34: \*

Database sequences: 240622  
Search time (sec): 71.600000

Search time (sec): 94.055609

score\_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
N_Geneseq_34:v31981	+	8841.00	15057.19	6604	!	Human Down syndrome-cell adhesion molecule
N_Geneseq_34:v31988	+	8483.00	14446.00	0.0	6413	Human Down syndrome-cell adhesion molecule
N_Geneseq_34:v31987	+	1742.50	2944.16	1.7e-156	2173	Mouse Down syndrome-cell adhesion molecule
N_Geneseq_34:v27207	+	1351.50	2280.32	1.6e-119	1493	CDNA clone ethb0118f2 encoding
N_Geneseq_34:v31985	+	1071.00	1807.34	3.5e-93	842	Mouse Down syndrome-cell adhesion molecule
N_Geneseq_34:v31986	+	880.50	1481.25	5.1e-75	898	Mouse Down syndrome-cell adhesion molecule
N_Geneseq_34:080196	+	653.00	1075.12	2.1e-52	4608	Deleted in colorectal carcinoma
N_Geneseq_34:012752	+	651.00	1070.43	3.9e-52	5186	Human Down syndrome-cell adhesion molecule
N_Geneseq_34:v31982	+	609.00	1026.51	1.1e-49	388	Human contactin coding sequence
N_Geneseq_34:107313	+	562.00	922.95	6.4e-44	3395	Human contactin coding sequence
N_Geneseq_34:074440	+	560.00	919.65	9.8e-44	3360	Human contactin cDNA (EMBL Acc
N_Geneseq_34:086478	+	546.50	890.37	4.2e-42	6000	PRP-OB Protein tyrosine phosphatase
N_Geneseq_34:1885389	+	546.50	890.37	4.2e-42	6000	Human protein tyrosine phosphatase
N_Geneseq_34:V40887	+	531.50	866.41	1.2e-40	6254	Coding sequence of clone C0722
N_Geneseq_34:162739	+	524.50	857.15	3.0e-40	3997	Human neural cell adhesion molecule
N_Geneseq_34:v40528	+	505.00	825.45	1.7e-38	3442	Human sapiens DLB5_1 clone sec
N_Geneseq_34:086902	+	408.50	655.22	5.2e-29	5690	Rat receptor type-protein tyrosine kinase
N_Geneseq_34:115928	+	383.00	620.71	4.4e-27	2450	Neural cell adhesion molecule
N_Geneseq_34:1745351	+	384.50	617.34	5.7e-27	4258	Human colon carcinoma kinase 4
N_Geneseq_34:V19872	+	358.00	572.75	2.1e-24	3976	Human sapiens cdo tumour suppressor gene
N_Geneseq_34:124310	+	355.00	572.75	2.1e-24	3997	Human cell adhesion molecule
N_Geneseq_34:T15929	+	348.50	563.04	7.1e-24	2178	Rattus norvegicus cdo tumour suppressor gene
N_Geneseq_34:V19870	+	317.50	499.50	2.5e-20	6039	Rattus norvegicus cdo tumour suppressor gene
N_Geneseq_34:094313	+	280.50	453.28	9.3e-18	1200	Tyrosine phosphatase M6P-Belt
N_Geneseq_34:N81584	+	283.00	443.24	1.8e-17	2839	11V7 cDNA encoding carcinogen
N_Geneseq_34:094311	+	283.00	443.24	3.4e-17	4555	Tyrosine phosphatase M6P-delta
N_Geneseq_34:071557	+	277.00	441.66	4.1e-17	2031	Carcinoembryonic antigen DNA
N_Geneseq_34:0543495	+	277.00	441.51	4.2e-17	2059	Immunogenic carinoembryonic antigen
N_Geneseq_34:0543492	+	279.00	441.48	4.2e-17	2839	Carinoembryonic antigen CEA-C
N_Geneseq_34:045062	+	279.00	441.48	4.2e-17	2097	Carinoembryonic antigen CEA-B
N_Geneseq_34:082807	+	277.00	441.32	4.3e-17	2270	Carcinoembryonic antigen gene
N_Geneseq_34:057868	+	277.00	440.10	5.0e-17	2349	H6/CEA expression cassette frc
N_Geneseq_34:T57543	+	277.00	437.74	5.3e-17	2348	Human carcinembryonic antigen
N_Geneseq_34:T77551	+	277.50	428.25	2.3e-16	2839	Human fibronectin cDNA. New fibronectin cDNA sequence encoding human fibronectin gene. New file
N_Geneseq_34:N02780	+	271.00	427.82	2.4e-16	421.38	Sequene encoding human fibronectin gene. New file
N_Geneseq_34:N70596	+	273.50	5.5e-16	7705	Rattus norvegicus cdo tumour	
N_Geneseq_34:Q15214	+	272.50	419.67	5.9e-16	7705	Rattus norvegicus Class II tumour
N_Geneseq_34:V19871	+	270.00	418.66	7.9e-16	5688	Rabbit ATHERO-ELAM. New endothelial
N_Geneseq_34:V19008	+	270.00	418.66	7.9e-16	5688	Rabbit ATHERO-ELAM. New endothelial
N_Geneseq_34:013635	+	260.00	410.45	2.3e-15	2487	Rabbit ATHERO-ELAM. New endothelial

N_Geneseq_34:N81611	+	261.00	410.41	2.3e-15	2928	Carcinoembryonic antigen
N_Geneseq_34:v19007	+	263.50	406.93	3.5e-15	6030	Rattus norvegicus Class II
N_Geneseq_34:Q05502	+	262.50	402.59	6.2e-15	7705	Sequence encoding human file

#### seq\_documentation\_block:

ID: v31981 standard; cDNA: 6604 BP.

AC: V31981;

DT: 20-SEP-1998 (first entry)

DE: Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.

DS-CAM1: Down syndrome-cell adhesion molecule; neural cell;

KW: signal transduction; trisomy 21; mental retardation;

holoprosencephaly; corpus callosum agenesis;

schizencephaly; diagnosis; assay; human; ds; ss;

OS: Homo sapiens.

Key: Location/Qualifiers

FT: CDS

FT: sig-peptide

FT: mat\_peptide

FT: /tag= c

FT: W09817705-A1.

FT: 30-APR-1998.

FT: 23-OCT-1997; U19547.

FT: 25-OCT-1996; US-029322.

FT: PA (CEDARS SINAI MEDICAL CENT.

FT: Korenberg JR;

DR: W42086.

P-PSDB: New isolated Down's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities

Claim 3, Page 65-72; 10pp; English.

This cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAM1 (see W42086), a cell surface glycoprotein belonging to a novel subclass of the Ig superfamily with higher homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and pI artificial chromosomes between ERS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see V31982), was obtained and used to screen a trisomy 21 human foetal brain (14 wk gestation) cDNA library. Further clones were obtained by exon trapping. The complete DS-CAM1 cDNA sequence was deduced from overlapping clones. A splice variant cDNA (see V31988), encoding non-membrane bound DS-CAM2 (see W42087), was also identified. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome 21q22.2-22.3. The invention also provides murine DS-CAM partial sequences (see V31985-87), expression vectors and host cells, transgenic animals, antisense oligonucleotides, and primers useful for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as down syndrome, mental retardation, holoprosencephaly, genesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides are used for inhibiting translation of mRNA. Sequence 6604 BP: 1673 A; 1827 C; 1768 G; 1336 T;

align\_scores:

Quality: 8841.00

Length: 1910

Gaps: 0

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-08-956-991-2 v31981 ..

Align seg 1/1 to: V31981 from: 1 to: 6604

1 MetProIleLeuAlaLeuSerLeuLeuPheGlnSerPheAlaAsnValPheSe 17  
 ||||||| 1353 ATCTGCTAAAGGGATAGGCCGCCTGTACGGAAACGCCACTGAAAGCCAC 1402  
 453 ATGTTGATACTGGCTCTCCTCTGTTCCAGAGCTTCCGAATGTTTCAG 502  
 17 rGlusPheLeuHisSerSerLeuLeuPheAlaAsnAlaLeuLeuGlu 34  
 ||||||| 503 TGAGGACTCTACACTCCACGCTCTACTTGTCATGCACTCTGCAAGAGG 552  
 34 alvalPheAlaSerThrThrGlyLysLeuValProCysProAlaAlaGly 50  
 ||||||| 553 TAGTTGTCGACGACCACGGGACTCTGTCGCTGCCCGAGCACAGGC 602  
 67 rAspValProGlyLeuArgLysValHisProAspGlyThrLeuGlyLeu 44  
 ||||||| 553 CGATGTCGCCCGGATTCGCCAGTCGTACCCCAACGGCACTTCGAATT 702  
 51 IleProProValThrLeuArgTrpTyroLeuAlaThrGlyGluGluIleTy 67  
 ||||||| 603 ATCCCTCTGTGACTCTCAGATGGTACCTAGCCACGGGAGGAGCTCA 652  
 84 heProPheProProSerSerPheSerThrLeuIleHisAspThrTyr 100  
 ||||||| 703 TCCCTTCCTCTCAACTGCTAACCTTAATCATGA AACATAT 752  
 101 TYRCYrThrAlaGluAsnProSerGlyLysIleArgSerGlnAspValH 117  
 ||||||| 703 TATTCGACAGCTGAAATCTCTCAGGGAAATTAGTCAGGATGTCAGGATGTC 802  
 117 sIleLeuAlaValLeuArgGluProIrrThrValArgValGluAspGlnI 134  
 ||||||| 803 CATCAAGCTGTTTACGGGACCCCTATACGTCCTGTCGGAGGACCA 852  
 134 ysthreMetArgLysAsnValAlaValAlaPhelysCysIleLeuProSer 150  
 ||||||| 853 AAACCATGAGGCCATGTGGGCTCAACTGCTATCCCCTCG 902  
 151 ValGluIalArylLeuLeuValSerTrpGlyLysAspThrValSerLe 167  
 ||||||| 903 CTGGAGGGCTACATCCTACTGTCGTCCTCAGGGAGAACGACTGTTCACT 952  
 167 uVaSerGlySerArgPheLeuIleThrSerThrGlyAlaLeuThrIle 184  
 ||||||| 953 TGTCTAGAGTCAGATTCTCATCACATCCACGGGAGCCTGTATTA 1002  
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 217 lSeAspProAlaAsnSeAlaProSerIleLeuAspGlyPheAspHsA 234  
 ||||||| 1103 ATCAGACCCAGCGACTCAGCCCCATCTACTGATGGTGTGACATC 1152  
 234 rGlySAlaMetAlaIgLyGlnArgValGluLeuProCysLysAlaLeuGly 250  
 ||||||| 1153 GCAAGCCATGCTGCGACGTGGCTGGCTGGCTCAAGGCCCTCGG 1202  
 251 HisProGluProAspTyArgPheLeuLysAspAsnMetProLeuGlu 267  
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 267 uSerGlyIargPheGlnLysThrValThrGlyLeuLeuIleGluAsnIea 284  
 ||||||| 1253 TTCAAGGGAGTTCAGAAGACCGCTGACGGGGCTCTCATGAGACATC 1302  
 284 rGProSerAspSerGlySerTyValCysGluValSerAsnArgTyGly 300  
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 334 eCysSerValThrGlyLysGluAspGlyInlieLeuSerTrpTirArgAsn 350  
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 367 sGluAspLeuIleMetAspHisMetValLysSerAspGlyGlyAlaTyR 384  
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 417 lValSerProAlaIgLuProValSerLeuMetCysasnValysGlyThr 434  
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 451 GlySerHisArgLysArgInlieIleThrSerGlyLysValnValse 467  
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 467 rTyLeuAsnIleSerSe ..rGlnValArgSpGlyGlyIlyValTyArg 484  
 1853 CTACTGGAACATCCACSTCCACGGTGGACGGAGCTACCGCT 1902  
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 1903 GCACGCCAACACTCGGGGAGCTGCTCTGTGTCCTGTCGATAAAC 1952  
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 2003 KGAGCGGGACACATCACATCCTGCTGATGGCTATCCCTATTACT 2052  
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 2203 CCACCAAGCCAGAGCGTCACCGTGGAGTCACGTCACAGTCCACAGTACGCA 2252  
 601 ProPheGluIupeProArgPheSerIleGlyGlnIalGlyValPheIleProcy 617

Date: Jul 23, 1999 12:09 PM  
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out\_format : pif

549 glnValAlaPheGluAsnAsnGlyThrLeu..... LysLeuSerA 563  
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 595 I-Pro.. ProHeleGlnProHeleGluProArgPheSerIleGly 611  
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 414 ACCACTGAGGTCTTTCACAGACAGAACTCATGCCATGGAG 463  
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